

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:15 ; Search time 63.43 Seconds
(without alignments)
679.107 Million cell updates/sec

Title: US-09-502-984B-37
Perfect score: 1284
Sequence: 1 KFSKALLAARGPEELICFRKNRLEEEVERLKLQVGER 249

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	903.5	70.4	509	6 Q9MYZ9	Q9MYZ9 sus scrofa
2	888	69.2	316	11 Q35545	Q35545 ratius norv
3	782	60.9	229	6 Q27930	Q27930 bos indicus
4	778	60.6	229	6 Q28206	Q28206 bos taurus
5	719.5	56.0	387	6 Q95N13	Q95N13 ovis aries
6	719.5	56.0	418	6 Q95N14	Q95N14 ovis aries
7	152	11.8	566	11 Q925F5	Q925F5 mus musculu
8	133.5	10.4	422	4 Q75462	Q75462 homo sapien
9	132.5	10.3	422	4 Q9UHS5	Q9UHS5 homo sapien
10	128.5	10.0	425	11 Q9JMS8	Q9JMS8 mus musculu
11	118	9.2	296	6 Q18880	Q18880 bos taurus
12	114.5	8.9	521	4 Q96TF0	Q96TF0 homo sapien
13	112.5	8.8	581	6 Q46561	Q46561 ovis aries
14	112.5	8.8	634	6 Q46600	Q46600 bos taurus
15	111.5	8.7	626	13 Q90MG7	Q90MG7 cynops pyr
16	108	8.4	35	3 Q96UT3	Q96UT3 saccharomyc

17	107	8.3	608	6 Q9N0Y7	Q9N0Y7 monodelphis
18	106.5	8.3	611	13 Q9PT9	Q9PT9 xenopus lae
19	105.5	8.2	638	6 Q95TF2	Q95TF2 alluropoda
20	102.5	8.0	628	11 Q9UKT1	Q9UKT1 cavia porce
21	102.5	8.0	628	11 Q9JUG1	Q9JUG1 cavia porce
22	102.5	8.0	628	11 Q9J197	Q9J197 cavia porce
23	102	7.9	638	6 Q9U69	Q9U69 canis faml
24	101.5	7.9	848	6 Q9WZS2	Q9WZS2 sus scrofa
25	99.5	7.7	1165	6 Q02671	Q02671 sus scrofa
26	99.5	7.7	1469	5 Q9U190	Q9U190 leishmania
27	99	7.7	622	6 Q9N0J7	Q9N0J7 callithrix
28	99	7.7	894	6 Q9MYL1	Q9MYL1 macaca mula
29	99	7.7	925	6 Q9MYK9	Q9MYK9 macaca mula
30	99	7.7	1163	6 Q9MYL2	Q9MYL2 macaca mula
31	99	7.7	1194	6 Q9MYT0	Q9MYT0 macaca mula
32	98.5	7.7	538	4 Q9HBE5	Q9HBE5 homo sapien
33	98.5	7.7	538	4 Q9HB91	Q9HB91 homo sapien
34	96.5	7.5	390	4 Q9UEH7	Q9UEH7 homo sapien
35	96.5	7.5	1093	11 Q70535	Q70535 ratius norv
36	96.5	7.5	1627	5 Q96200	Q96200 giardia lam
37	96	7.5	896	4 Q92919	Q92919 homo sapien
38	96	7.5	896	4 Q13594	Q13594 homo sapien
39	96	7.5	906	4 Q13593	Q13593 homo sapien
40	96	7.5	958	4 Q92920	Q92920 homo sapien
41	96	7.5	958	4 Q13592	Q13592 homo sapien
42	96	7.5	1165	4 Q92921	Q92921 homo sapien
43	95.5	7.4	611	13 Q91BR6	Q91BR6 xenopus lae
44	95.5	7.4	611	13 Q9PT10	Q9PT10 xenopus lae
45	95.5	7.4	636	13 Q90Z16	Q90Z16 paralicthy

ALIGNMENTS

RESULT	ID	Q9MYZ9	PRELIMINARY:	PRT:	509 AA.
AC	Q9MYZ9;	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)				
DE	ERYTHROPOIETIN RECEPTOR.				
DE	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_Taxid=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER;				
RA	Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,				
RA	Christenson R.K., Vallet J.L.,				
RT	"Porcine Erythropoietin Receptor: Molecular Cloning and Expression in				
RT	Embryonic and Fetal Liver."				
RT	Domest. Anim. Endocrinol. 0:0-0(2000).				
DR	EMBL: AF274305; AAF77065.1; -.				
DR	HSSP: P19235; 1EBA.				
DR	InterPro: IPR002996; CRA.				
DR	InterPro: IPR000572; Euk_Oxidored_molzb.				
DR	InterPro: IPR003961; FN_III.				
DR	InterPro: IPR003528; Hematopo_receptor_L_F1.				
DR	Pfam: PF00041; fn3; 1.				
DR	SMART: SM00060; FN3; 1.				
DR	PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.				
DR	PROSITE: PS00559; MOLYDOPTERIN_EUK; UNKNOWN_1.				
KW	RECEPTOR.				
SQ	SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCD8A CRC64;				

Query Match 70.4%; Score 903.5; DB 6; Length 509;
Best Local Similarity 80.2%; Pred. No. 2.5e-71;
Matches 170; Conservative 18; Mismatches 23; Indels 1; Gaps 1;

QY 1 KFSKALLAARGPEELICFTEFLDLVCFEEASAGVGNGFSFQLEDEPWKICRL 60

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Db      34  KFSKALLAARPEELCTERLEEDLVCFWEAGSAGVPEDEYSFSEQLEGEPMKCHL 93
Qy      61  HQAPTARCAIRFCISLPTADTSSFVPLELRLT-AASGAPFRHVIHINEVLLDAPVGLV 119
Db      94  HQAPTARCAIRFCISLPTADTSSFVPLELRLTAVTESSGAPFRHVIHINEVLLDAPVGLV 153
Qy      120  ARLADESGHVIVRWLPPETPMTSHIRFELDLSAGNGAGSVORVELLEGRTCVLSNLRG 179
Db      154  ARAEESGHVIVRWLPPPGAPMASLIRVEVNIHSTENAGAGVQREILDGRTCVLSNLRG 213
Qy      180  RRTITAVRARMAEPSFGFWSAMSEPVSLT 211
Db      214  GRTYTFVRRARMAEPSFGFWSAMSEPVSLT 245

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RESULT 2
035545  PRELIMINARY; PRT; 316 AA.
ID 035545;
AC 035545;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTRON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR PRECURSOR.
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=98292611; PubMed=9630610;
RA Yamae I R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,
RA Miyake K., Nakano Y.;
RT "The intron 5-inserted form of rat erythropoietin receptor is
RT expressed as a membrane-bound form."
RL Biochim. Biophys. Acta 1403:169-178(1998).
DR EMBL; D83509; BAA22373.1; -.
DR HSSP; P19235; IEBA.
DR InterPro; IPR002996; CRAA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 316 POTENTIAL.
SQ SEQUENCE 316 AA; 34220 MW; 05C44BF8516C180B CRC64;

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Query Match 69.2%; Score 888; DB 11; Length 316;
 Best Local Similarity 75.1%; Pred. No. 3.2e-70;
 Matches 169; Conservative 24; Mismatches 22; Indels 10; Gaps 2;

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Qy      1  KFSKALLAARPEELCTERLEEDLVCFWEAGSAGVPEDEYSFSEQLEGEPMKCHL 60
Db      34  KFSKALLAARPEELCTERLEEDLVCFWEAGSAGVPEDEYSFSEQLEGEPMKCHL 92
Qy      61  HQAPTARCAIRFCISLPTADTSSFVPLELRLTAAAGAPFRHVIHINEVLLDAPVGLV 120
Db      94  HQAPTARCAIRFCISLPTADTSSFVPLELRLTAAAGAPFRHVIHINEVLLDAPVGLV 152
Qy      121  RLADESGHVIVRWLPPETPMTSHIRFELDLSAGNGAGSVORVELLEGRTCVLSNLRG 180
Db      153  RRAEESGHVIVRWLPPPGAPMASLIRVEVNIHSTENAGAGVQREILDGRTCVLSNLRG 212
Qy      181  RRTITAVRARMAEPSFGFWSAMSEPVSLT-----GGGGS 216
Db      213  TRTYTFVRRARMAEPSFGFWSAMSEPVSLTASGATVPVGGGA 257

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RESULT 3
 Q27950

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ID 027950  PRELIMINARY; PRT; 229 AA.
AC 027950;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EFOR.
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U61398; AAB03870.1; -.
DR HSSP; P19235; IEBA.
DR InterPro; IPR002996; CRAA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25196 MW; F6E01C4AB07893E8 CRC64;

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Query Match 60.9%; Score 782; DB 6; Length 229;
 Best Local Similarity 78.5%; Pred. No. 4.6e-61;
 Matches 146; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

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Qy      26  DLYCFEENASAGVGNFSEFQLEDEPMKICRLHQAPTARCAIRFCISLPTADTSSFV 85
Db      1  DLYCFEENATAGVGNFSEFQLEGEPMKICRLHQAPTARCAIRFCISLPTADTSSFV 60
Qy      86  PLELRRLTAASGAPFRHVIHINEVLLDAPVGLVARLADESGHVIVRWLPPETPMTSHI 145
Db      61  PLELRRLTAASGAPFRHVIHINEVLLDAPVGLVARLADESGHVIVRWLPPPGAPMASLI 120
Qy      146  RFLDLSAGNGAGSVORVELLEGRTCVLSNLRGRTITAVRARMAEPSFGFWSAMSE 205
Db      121  RVEVNIHSTENAGAGVQREILDGRTCVLSNLRGRTITAVRARMAEPSFGFWSAMSE 180
Qy      206  PVSLT 211
Db      181  PASLT 186

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RESULT 4
028206  PRELIMINARY; PRT; 229 AA.
ID 028206;
AC 028206;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EFOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U61399; AAB03871.1; -.
DR HSSP; P19235; IEBA.

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DB 18 SODVFLALATGEPLNCFOSQFFEDLTGFWDEEAA--PSGTYYOLLYAVRGKPRACPLYSQ 75
OY 64 PTARGAIREWCSLPTAD-TSSFVPLELRLTAAS-GAPRFHVIHI-----NE 108
DB 76 SVTFEGTRYVCOFPADDEVNLFPPHLHMKVANSVLTLLIOLVLEFVDSVETCCPTLMNPN 135
OY 109 VLLDAPVGLVARLADESGHVIRMLPPETPMTSHIRFELDISAGNGAGSVORVELLEG 168
DB 136 VPVLDDP-PCVHPPTASOP-HGVRTSPAGAPF-----LTVKGS- 173
OY 169 RTECVLSNLRGRTITIAVARARAEPSFGFSWAMSEPVSL 209
DB 174 ---CLVSGLOAGRSYWLQKSPDPVGLRSGMGPSPPTV 211

RESULT 8
OY 075462 PRELIMINARY; PRT: 422 AA.
AC 075462;
DT 01-NOV-1998 (TREMblrel, 08, Created)
DT 01-NOV-1998 (TREMblrel, 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Welis T.N.C., Kosco-Villbois M.H., Gauchat J.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology with Members of the
RT Cytokine Type-1 Receptor Family.";
RL J. Immunol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangas F., Jacques Y., Minville S.;
RT "Cloning and expression of a novel soluble protein containing
RT hematopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF059293; AAC28335.1; -
DR EMBL: AF073515; AAD39681.1; -
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR Pfam: PR00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
KW Signal; Receptor.
FT SIGNAL. 1 37
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; AD9DEFB01B8428 CRC64;

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Query Match 10.4%; Score 133.5; DB 4; Length 422;
Best Local Similarity 23.7%; Pred. No. 0.0012;
Matches 64; Conservative 37; Mismatches 98; Indels 71; Gaps 16;

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OY 14 PEEELCTERLEEDLVCFEEFAASAGVPG-----NFSFQLEDEPW---KICRL 60
DB 138 PVNISCKSMKMDLTCRMT-----PGAHGFTPLHTNLSLYKLR--WYGQDNTCEE 186
OY 61 HQAPTARGAIREWCSLPTADTSSFPVLELRLTAAS--GAPRFH-RVHINEVLLDAPV 117
DB 187 YHTVGHHS-----CHIP-KDLAFTPEIVEATNRLGSAKSDVLLDILDVTTDPPPD 240
OY 118 L-VARLADESGHVIRMLPPET-----PMTSHIRFELDISAGNGAGSVORVELLEG 171
DB 241 VHSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVEDSV-----DMKVVDVDSNQS 295
OY 172 CVLSNLRGRTITIAVARARAEPSFG-----GFSWAMSEPVSLT-----GGGGSRM 218

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DB 296 CRLAGLKPGTVIVVOYRCN-----PFGIYSKKAGINSEMSHPAATPSRERPGGAGC 351
OY 219 EKLEQKVKELLRKNERLEEVEER-LKQLVG 247
DB 352 EP-----RGEPSSGPVRRELKQFLG 372

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RESULT 9
OY 090HH5 PRELIMINARY; PRT: 422 AA.
AC 090HH5;
DT 01-MAY-2000 (TREMblrel, 13, Created)
DT 01-MAY-2000 (TREMblrel, 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jelmeberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehnert J.M., O'Hara P.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF178684; AAD54385.1; -
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR Pfam: PR00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

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```

Query Match 10.3%; Score 132.5; DB 4; Length 422;
Best Local Similarity 23.7%; Pred. No. 0.0015;
Matches 64; Conservative 37; Mismatches 98; Indels 71; Gaps 16;

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OY 14 PEEELCTERLEEDLVCFEEFAASAGVPG-----NFSFQLEDEPW---KICRL 60
DB 138 PVNISCKSMKMDLTCRMT-----PGAHGFTPLHTNLSLYKLR--WYGQDNTCEE 186
OY 61 HQAPTARGAIREWCSLPTADTSSFPVLELRLTAAS--GAPRFH-RVHINEVLLDAPV 117
DB 187 YHTVGHHS-----CHIP-KDLAFTPEIVEATNRLGSAKSDVLLDILDVTTDPPPD 240
OY 118 L-VARLADESGHVIRMLPPET-----PMTSHIRFELDISAGNGAGSVORVELLEG 171
DB 241 VHSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVEDSV-----DMKVVDVDSNQS 295
OY 172 CVLSNLRGRTITIAVARARAEPSFG-----GFSWAMSEPVSLT-----GGGGSRM 218
DB 296 CRLAGLKPGTVIVVOYRCN-----PFGIYSKKAGINSEMSHPAATPSRERPGGAGC 351
OY 219 EKLEQKVKELLRKNERLEEVEER-LKQLVG 247
DB 352 EP-----RGEPSSGPVRRELKQFLG 372

RESULT 10
OY 090JMS8 PRELIMINARY; PRT: 425 AA.
AC 090JMS8;
DT 01-OCT-2000 (TREMblrel, 15, Created)
DT 01-OCT-2000 (TREMblrel, 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
DE CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.
GN CR1F1 OR CR1M3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;

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DB 269 WPGNTLVANSIFLLLTGPTTLFLKLSPRVKRIFYON 304

RESULT 13

046561 PRELIMINARY: PRT: 581 AA.

AC 046561; P79205; 046573; P79203; 046569;

DT 01-JUN-1998 (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (PRLR) (OPR).

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC TISSUE=MAMMARY GLAND, AND LIVER.

RX MEDLINE=98001468; PubMed=9343303;

RA Bignon C., Bihart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;

RT "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents.";

RL J. Mol. Endocrinol. 19:109-120(1997).

RN [2]

RP SEQUENCE OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING.

RC STRAIN=SCOTTISH BLACKFACE / ISOLATE M22/80; TISSUE=ANTERIOR PITUITARY;

RX MEDLINE=99049302; PubMed=9832462;

RA Tortorese D.J., Brooks J., Ingleton P.M., Mcneilly A.S.;

RT "Detection of prolactin receptor gene expression in the sheep pituitary gland and visualization of the specific translation of the signal in gonadotrophs.";

RL Endocrinology 139:5215-5223(1998).

RN [3]

RP SEQUENCE OF 147-302 FROM N.A., AND ALTERNATIVE SPLICING.

RC TISSUE=FETAL LIVER, AND CORPUS LUTEUM;

RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;

RT "Two forms of the prolactin receptor messenger ribonucleic acid are present in ovine fetal liver and adult ovary.";

RL Endocrine 3:291-295(1995).

CC -1- PUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS: LONG ISOFORM (L-OPR) (SHOWN HERE), SHORT ISOFORM (S-OPR) AND SOLUBLE ISOFORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (LIVER, PITUITARY, ADRENAL GLAND, OVARY AND FETAL LIVER).

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC EMBL; AF041257; AAB96795.1; -

DR EMBL; AF041977; AAB96920.1; -

DR EMBL; AF041979; AAB97082.1; -

DR EMBL; AF042358; AAB97744.1; -

DR EMBL; AF042358; AAB97743.1; -

DR EMBL; AF041978; AAB96965.1; -

DR EMBL; Y10578; CAA71597.1; -

DR EMBL; Y10808; CAA71766.1; -

DR HSSP; P14787; 1AN3.

DR InterPro: IPR002996; CRIA.

DR InterPro: IPR003961; FN_III.

DR InterPro: IPR003528; Hematopo_receptor_L_FL.

DR Pfam: PF00041; fn3; 2.

DR SMART: SM00060; FN3; 2.

DR PROSITE: PS01352; HEMATOPO_REC_L_FL; UNKNOWN.1.

KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat;

KW Alternative splicing.

FT SIGNAL 1 24 . POTENTIAL.

FT CHAIN 25 581 . PROLACTIN RECEPTOR.

FT DOMAIN 25 237 . EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 238 258 . POTENTIAL.

FT DOMAIN 259 581 . CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 122 FIBRONECTIN TYPE-III.

FT DOMAIN 123 227 FIBRONECTIN TYPE-III.

FT DISULFID 36 46 BY SIMILARITY.

FT DISULFID 75 86 BY SIMILARITY.

FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPPLIC 24 66 GOSPEKRLINCRSGKRTFCWMPRGADGGLPNTVTLTY

FT VARSPPLIC 67 581 YLLLVTS (IN SOLUBLE ISOFORM).

FT VARSPPLIC 286 296 MISSING (IN SOLUBLE ISOFORM).

FT VARSPPLIC 297 581 MISSING (IN SHORT ISOFORM).

FT CONFLICT 281 281 I -> V (IN AAB97743 AND AAB97744).

FT CONFLICT 387 387 E -> K (IN REF. 2).

SQ SEQUENCE 581 AA; 65235 MW; EC534FDE538837A0 CRC64;

Query Match 8.8%; Score 112.5; DB 6; Length 581;

Best Local Similarity 22.2%; Pred. No. 0.13;

Matches 49; Conservative 41; Mismatches 100; Indels 31; Gaps 11;

QY 6 AALLAARGPE---LLCFERLELDVCFPEEASAGVGNGFSFQLEDEPMKLCRLH 61

DB 19 ASLLNGSPPEKRLIKCNKSPGKETTCWPEPADGGL-PTNTLYLRKEG---TLIH 73

QY 62 QAPFARGAIRFWCSLPTADTSFVPLELRJTA-----ASGAPRFRHVININEVLLDAP 115

DB 74 ECDVDYKGTGPNNSCYFSKSKYISIMKMYIVTSALNOMGISSDPLY---VDVTIVEPEPP 130

QY 116 VGLVARL---ADSGHVVIRMLPPETPTMS---HIRELDISAGAGAGVQVYELLEGR 169

DB 131 VNLTLELKHEDRKRPYLMKWSPEPTLDVKSQYELRLPERATD--WETHAPAKL 188

QY 170 TECVLNLRGRTRTITAVRARMAEPSPGFWMSAPSVSL 210

DB 189 TOLKINLIPGQKYLVOIRCK---PDH-GYWSMS-PESTI 224

RESULT 14

046600 PRELIMINARY: PRT: 634 AA.

AC 046600;

DT 01-JUN-1998 (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, last annotation update)

DE SOMATOTROPIN RECEPTOR 1B PRECURSOR.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HOLSTEIN;

RA Lucy M.C., Boyd C.K.;

RT "Bovine somatotropin receptor 1B mRNA.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF044258; AAC02534.1; -

DR HSSP; P10912; 1A22.

DR InterPro: IPR002996; CRIA.

DR InterPro: IPR003961; FN_III.

DR InterPro: IPR003528; Hematopo_receptor_L_FL.

DR Pfam: PF00041; fn3; 1.

DR SMART: SM00060; FN3; 1.

DR PROSITE: PS01352; HEMATOPO_REC_L_FL; UNKNOWN.1.

KM Signal; Receptor.

FT SIGNAL 1 18 . POTENTIAL.

FT CHAIN 19 634 . SOMATOTROPIN RECEPTOR 1B.

SQ SEQUENCE 634 AA; 70914 MW; 176936D32EA7C4C9 CRC64;

Query Match 8.8%; Score 112.5; DB 6; Length 634;

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